



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 01:32 am BST

PDB ID : 5X55
Title : Crystal structure of mimivirus uracil-DNA glycosylase
Authors : Kwon, E.; Pathak, D.; Kim, D.Y.
Deposited on : 2017-02-14
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

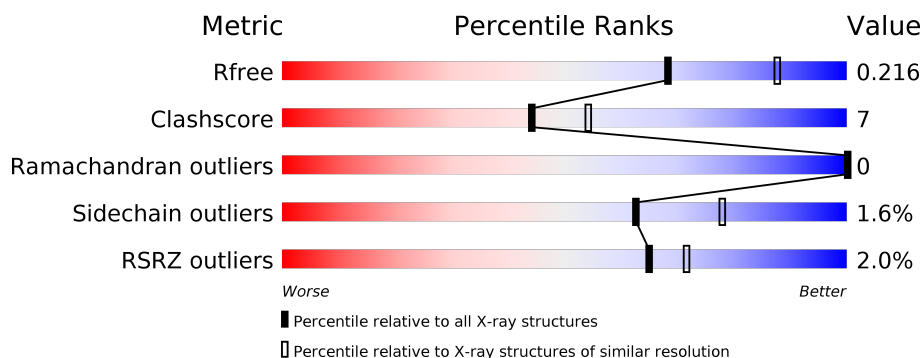
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	370	<div> <div> <div></div> <div>62%</div> <div>13%</div> <div>25%</div> </div> <div> <div></div> <div>62%</div> <div>13%</div> <div>25%</div> </div> </div>
1	B	370	<div> <div> <div></div> <div>63%</div> <div>11%</div> <div>25%</div> </div> <div> <div></div> <div>63%</div> <div>11%</div> <div>25%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4814 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.



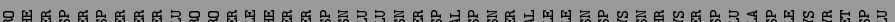
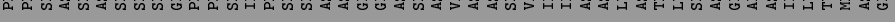




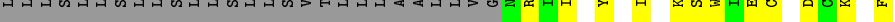





















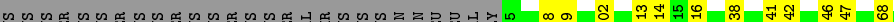
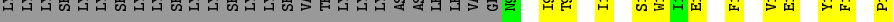

























- Molecule 1 is a protein called Probable uracil-DNA glycosylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	0	0
			2247	1466	371	397	13			
1	B	276	Total	C	N	O	S	0	0	0
			2247	1466	371	397	13			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	176	Total	O	0	0
			176	176		
2	B	144	Total	O	0	0
			144	144		

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Chain A: 
- Chain B: 
- Chain C: 
- Chain D: 
- Chain E: 
- Chain F: 
- Chain G: 
- Chain H: 
- Chain I: 
- Chain J: 
- Chain K: 
- Chain L: 
- Chain M: 
- Chain N: 
- Chain O: 
- Chain P: 
- Chain Q: 
- Chain R: 
- Chain S: 
- Chain T: 
- Chain U: 
- Chain V: 
- Chain W: 
- Chain X: 
- Chain Y: 
- Chain Z: 
- Chain AA: 
- Chain AB: 
- Chain AC: 
- Chain AD: 
- Chain AE: 
- Chain AF: 
- Chain AG: 
- Chain AH: 
- Chain AI: 
- Chain AJ: 
- Chain AK: 
- Chain AL: 
- Chain AM: 
- Chain AN: 
- Chain AO: 
- Chain AP: 
- Chain AQ: 
- Chain AR: 
- Chain AS: 
- Chain AT: 
- Chain AU: 
- Chain AV: 
- Chain AW: 
- Chain AX: 
- Chain AY: 
- Chain AZ: 
- Chain BA: 
- Chain BB: 
- Chain BC: 
- Chain BD: 
- Chain BE: 
- Chain BF:
- Chain BG:
- Chain BH:
- Chain BI:
- Chain BJ:
- Chain BK:
- Chain BL:
- Chain BM:
- Chain BN:
- Chain BO:
- Chain BP:
- Chain BQ:
- Chain BR:
- Chain BS:
- Chain BT:
- Chain BU:
- Chain BV:
- Chain BW:
- Chain BX:
- Chain BY:
- Chain BZ:
- Chain CA:
- Chain CB:
- Chain CC:
- Chain CD:
- Chain CE:
- Chain CF:
- Chain CG:
- Chain CH:
- Chain CI:
- Chain CJ:

- Chain B:
-
- 290
- 63% 11% 25%
- SER GLU SER SER LYS LYS ASN VAL ASP PRO PHE SER ASP SER SER SER GLU PRO PRO ILE PHE SER SER ASP ASN GLU GLU ASN SER SER ASP VAL LEU VAL GLY N95 I98 T99 I102 S113 W114 E115 E116 F138 V141 E142 Y146 F147 P168 N173 V177
- D191 P192 S196 C197 I198 S199 G200 Y203 A204 W205 K219 K236 A257 T260 V261 L262 W263 S264 S265 G266 V267 D281 T284 Y287 D288 D289 F292 W295 K310 I313 S320 F321 Y322 S326 H350 L370

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	96.27Å 95.62Å 132.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.74 – 2.30 33.09 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.74-2.30) 99.8 (33.09-2.30)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.40 (at 2.31Å)	Xtriage
Refinement program	PHENIX (dev_2313: ???)	Depositor
R, R_{free}	0.173 , 0.216 0.174 , 0.216	Depositor DCC
R_{free} test set	1376 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	26.6	Xtriage
Anisotropy	0.414	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.035 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4814	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.14% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.46	0/2321	0.59	0/3156
1	B	0.46	1/2321 (0.0%)	0.56	0/3156
All	All	0.46	1/4642 (0.0%)	0.58	0/6312

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	361	ARG	CZ-NH1	-5.34	1.26	1.33

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2247	0	2222	31	0
1	B	2247	0	2220	29	0
2	A	176	0	0	6	1
2	B	144	0	0	3	1
All	All	4814	0	4442	59	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (59) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:289:ASP:OD1	1:B:361:ARG:NH1	2.09	0.86
1:B:284:THR:O	1:B:310:LYS:NZ	2.11	0.83
1:A:120:ASP:H	1:A:122:LYS:HZ1	1.40	0.70
1:A:349:ASP:OD2	2:A:401:HOH:O	2.09	0.69
1:B:98:ILE:HD11	1:B:177:VAL:HG22	1.73	0.69
1:B:116:GLU:O	2:B:402:HOH:O	2.11	0.67
1:B:261:VAL:HG22	1:B:264:GLU:HB2	1.76	0.66
1:A:355:ASN:OD1	2:A:402:HOH:O	2.16	0.61
1:A:120:ASP:H	1:A:122:LYS:NZ	2.00	0.59
1:B:141:VAL:HG23	1:B:146:TYR:OH	2.04	0.58
1:A:117:CYS:SG	1:A:168:PRO:HG2	2.44	0.56
1:B:236:LYS:HG3	2:B:453:HOH:O	2.06	0.56
1:A:163:ARG:HG3	2:A:469:HOH:O	2.06	0.56
1:A:180:PRO:HA	1:A:183:ILE:HD12	1.87	0.55
1:B:295:TRP:HE1	1:B:350:HIS:CD2	2.25	0.55
1:A:96:ARG:NH1	1:A:169:GLU:OE1	2.40	0.55
1:A:114:TRP:CD1	1:A:168:PRO:HD3	2.44	0.52
1:B:138:PHE:HA	1:B:141:VAL:HG12	1.91	0.52
1:A:284:THR:HG21	1:A:306:VAL:HG22	1.92	0.51
1:B:99:THR:HA	1:B:102:ILE:HG22	1.92	0.51
1:A:289:ASP:OD1	1:A:361:ARG:HG3	2.11	0.50
1:A:276:THR:O	1:A:280:ILE:HG12	2.12	0.49
1:B:192:PRO:HD3	1:B:257:ALA:O	2.11	0.49
1:B:261:VAL:HG13	1:B:267:VAL:HG21	1.93	0.49
1:A:196:SER:HB3	1:A:262:LEU:HD11	1.95	0.49
1:B:197:CYS:SG	1:B:203:TYR:CE1	3.06	0.49
1:B:287:TYR:O	1:B:310:LYS:HE2	2.14	0.48
1:B:370:LEU:O	2:B:403:HOH:O	2.19	0.48
1:A:288:ASP:OD2	1:A:310:LYS:NZ	2.47	0.47
1:B:142:GLU:HA	1:B:147:PHE:CG	2.49	0.47
1:A:339:LYS:HE3	1:B:281:ASP:OD2	2.16	0.46
1:A:157:TYR:HB2	1:A:164:ILE:HD11	1.98	0.46
1:B:192:PRO:HG2	1:B:260:THR:HG22	1.99	0.45
1:B:191:ASP:OD1	1:B:266:GLY:HA2	2.16	0.45
1:B:114:TRP:CD2	1:B:168:PRO:HG3	2.52	0.45
1:B:281:ASP:HA	1:B:284:THR:HG22	1.98	0.45
1:B:113:SER:OG	1:B:116:GLU:HG3	2.18	0.44
1:A:149:GLN:O	1:A:153:LYS:HG3	2.17	0.44
1:A:98:ILE:HD11	1:A:177:VAL:HG22	1.98	0.44
1:A:349:ASP:O	1:A:353:LYS:HG3	2.18	0.44
1:A:122:LYS:HG2	1:A:122:LYS:H	1.61	0.44
1:A:96:ARG:HB2	1:A:101:TYR:CE2	2.53	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:173:ASN:ND2	1:B:205:MET:O	2.51	0.43
1:B:102:ILE:HD12	1:B:102:ILE:HA	1.71	0.43
1:A:267:VAL:O	2:A:403:HOH:O	2.21	0.43
1:A:236:LYS:HE3	1:A:236:LYS:HB2	1.82	0.43
1:A:104:ILE:HG22	1:A:212:PRO:HB3	2.01	0.43
1:A:96:ARG:O	2:A:404:HOH:O	2.21	0.43
1:B:196:SER:HB3	1:B:262:LEU:HD11	2.00	0.43
1:B:219:LYS:HG2	1:B:321:PRO:HG3	1.99	0.42
1:A:138:PHE:O	1:A:142:GLU:HG3	2.18	0.42
1:A:318:HIS:CG	1:A:319:PRO:HD2	2.55	0.41
1:B:292:PHE:HB2	1:B:313:ILE:HD13	2.00	0.41
1:B:98:ILE:CD1	1:B:177:VAL:HG22	2.46	0.41
1:B:370:LEU:HD23	1:B:370:LEU:HA	1.74	0.41
1:A:112:LYS:HB3	1:A:116:GLU:HB2	2.01	0.41
1:A:235:ARG:NH1	2:A:415:HOH:O	2.53	0.41
1:A:295:TRP:CE2	1:A:345:PHE:HE2	2.39	0.41
1:A:113:SER:OG	1:A:116:GLU:HG3	2.20	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:447:HOH:O	2:B:403:HOH:O[6_445]	2.01	0.19

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	274/370 (74%)	269 (98%)	5 (2%)	0	100	100
1	B	274/370 (74%)	264 (96%)	10 (4%)	0	100	100
All	All	548/740 (74%)	533 (97%)	15 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	254/346 (73%)	252 (99%)	2 (1%)	81	91
1	B	254/346 (73%)	248 (98%)	6 (2%)	49	66
All	All	508/692 (73%)	500 (98%)	8 (2%)	62	78

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	239	LYS
1	A	320	SER
1	B	261	VAL
1	B	289	ASP
1	B	310	LYS
1	B	320	SER
1	B	325	SER
1	B	361	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	276/370 (74%)	-0.15	5 (1%) 68 74	14, 25, 42, 62	0
1	B	276/370 (74%)	-0.14	6 (2%) 62 69	18, 29, 46, 78	0
All	All	552/740 (74%)	-0.15	11 (1%) 65 71	14, 27, 45, 78	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	198	ILE	5.6
1	A	198	ILE	5.0
1	B	322	TYR	3.9
1	B	197	CYS	3.5
1	A	95	ASN	3.4
1	B	200	GLY	3.3
1	A	161	ARG	3.3
1	B	95	ASN	3.0
1	A	322	TYR	2.6
1	A	335	PRO	2.6
1	B	199	SER	2.3

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.